SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Keegan, Kathleen S.

    (ii) TITLE OF INVENTION: Novel CREBa Isoform

    (iii) NUMBER OF SEQUENCES: 10

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Marshall, Gerstein & Borun
        (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
        (C) CITY: Chicago
        (D) STATE: Illinois
        (E) COUNTRY: USA
        (F) ZIP: 60606

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 09/884,566
        (B) FILING DATE: 2001-06-19
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Williams Jr., Joseph A.
        (B) REGISTRATION NUMBER: 38,659
        (C) REFERENCE/DOCKET NUMBER: 27866/37497

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 312-474-6300
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3190 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 304..1866

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTTGG CTTCCTTTTG GATGCACAGC      60

CCGATTTAAC CCCTGCACCT TCCGCCCGAT CCCAGCAGGC TTGTCCTCCC CGGGGAGTCA     120

CAGATTTCCG AGGACAAGGG TCGCGTAGCC TTCGGCAGGG CTCTCCCGAG TTCCTGCTCC     180

AGTGCATAAG TTCCACGCGC GCACACGCCA AGTACACGGG GAGAAGCGTC TCACCGGCCC     240

GCGGCGGCTC TGCGCGGTCC CCTCCTGCCT CAGCATCCTC GGGCCTGCGC GGCGCCCACC     300
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GCC ATG GAG GTG CTG GAG AGC GGG GAG CAG AGC GTC CTG CAG TGG GAC        348
    Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp
    1                   5                   10                  15

CGC AAG CTG AGC GAG CTG TCA GAG CCC GGA GAG ACT GAG GCC CTC ATG        396
Arg Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met
                20                  25                  30

TAC CAC ACG CAC TTC TCG GAG CTC CTA GAC GAG TTT TCC CAG AAC GTC        444
Tyr His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val
            35                  40                  45

CTG GGT CAG CTC CTG AGT GAC CCT TTC CTC TCA GAG AAG AGC GAG TCA        492
Leu Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser
            50                  55                  60

ATG GAG GTG GAG CCA TCT CCA ACA TCA CCA GCG CCT CTC ATC CAG GCT        540
Met Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala
    65                  70                  75

GAA CAC AGC TAC TCT CTG AGC GAG GAG CCC CGG ACT CAG TCA CCA TTT        588
Glu His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe
80                  85                  90                  95

ACC CAT GCG GCT ACC AGC GAC AGC TTC AAT GAC GAG GAG GTG GAG AGT        636
Thr His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser
                100                 105                 110

GAA AAA TGG TAC CTG TCT ACA GAG TTT CCT TCA GCT ACC ATC AAG AAA        684
Glu Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys
                115                 120                 125

GAG CCA ATC ACA GAG GAG CAG CCC CCG GGA CTT GTC CCT TCT GTC ACT        732
Glu Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr
                130                 135                 140

CTG ACC ATC ACA GCC ATT TCC ACT CCT TTT GAA AAA GAA GAG TCC CCT        780
Leu Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro
    145                 150                 155

CTG GAT ATG AAT GCT GGG GGG GAC TCC TCA TGC CAG ACG CTT ATT CCT        828
Leu Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro
160                 165                 170                 175

AAG ATT AAG CTG GAG CCC CAC GAA GTG GAT CAG TTC TTA AAC TTC TCC        876
Lys Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser
                180                 185                 190

CCG AAA GAA GCC TCC GTG GAT CAA CTG CAC TTA CCA CCA ACA CCA CCC        924
Pro Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro
                195                 200                 205

AGT AGT CAC AGC AGT GAC TCT GAG GGC AGC TTG AGC CCC AAC CCA CGC        972
Ser Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg
            210                 215                 220

CTG CAT CCC TTC AGC CTG TCT CAG GCC CAC AGC CCT GTC AGA GCC ATG        1020
Leu His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met
    225                 230                 235

CCC CGG GGC CCC TCT GCC TTG TCC ACA TCT CCT CTC CTC ACA GCT CCA        1068
Pro Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro
240                 245                 250                 255

CAT AAG CTG CAG GGA TCG GGC CCC CTG GTC CTG ACA GAA GAG GAG AAG        1116
His Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys
            260                 265                 270
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AGG ACC CTG GTT GCC GAG GGC TAT CCC ATT CCC ACC AAG CTG CCT CTG        1164
Arg Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu
            275             280             285

ACA AAA TCT GAG GAG AAG GCC CTG AAG AAA ATC CGG AGA AAG ATC AAG        1212
Thr Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys
            290             295             300

AAT AAG ATT TCT GCC CAA GAA AGC AGG AGA AAG AAG AAA GAA TAC ATG        1260
Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met
    305             310             315

GAC AGC CTG GAG AAA AAA GTG GAG TCT TGT TCA ACT GAG AAC TTG GAG        1308
Asp Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu
320             325             330             335

CTT CGG AAG AAG GTG GAG GTG CTG GAG AAC ACC AAT AGG ACT CTC CTT        1356
Leu Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu
            340             345             350

CAG CAA CTT CAG AAG CTT CAG ACT TTG GTG ATG GGG AAG GTC TCT CGA        1404
Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg
            355             360             365

ACC TGC AAG TTA GCT GGC ACA CAG ACT GGC ACC TGC CTC ATG GTC GTT        1452
Thr Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val
            370             375             380

GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG        1500
Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly
            385             390             395

CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG        1548
Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu
400             405                 410             415

TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC        1596
Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile
            420             425             430

TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG TCG AGC CCA GCC TCA ACC        1644
Tyr Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr
            435             440             445

GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG        1692
Gly Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser
            450             455             460

TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC        1740
Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile
    465             470             475

TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG        1788
Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln
480             485             490             495

CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA        1836
His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val
            500             505             510

GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCTCC        1886
Glu Leu Glu Arg Arg Val Asn Ala Thr Phe
            515             520

TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTTCCCC TTCACCACTG GATCTCGAGG    1946

AGGAGATGGC TAGTGTTACG GCTCGAGACA GGAGGCCAGC CCAGGGGGTT CTGCTTATGT    2006
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GTCCCCGTGG CTCTCCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTTCT CTTACTGCCA    2066

TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTTT CCACCAATAG    2126

TGCCAAGAAG ACACTGCCTG ATTCTTCCCC GGGAGGAGTG ACTCCTCTGA AGAAGACATG    2186

ACTCATGTTC AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA    2246

GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCTGCAC    2306

TGAGAGGACC AAAGCGTCAT TGCAGTCTTC TCTCCACCCT GTACCCCGGA GTCCTGATTG    2366

GATGTCTGCA GAGGCAGATG GGGCTCCCAC CATATTTTCA GGCCGCAAGT GCAATTCCTG    2426

AAGGCATCAG GCTCTTCTCT CCCAGGCTCT CCTGCCCACT GTGTTGTTTG TAGGACACCC    2486

CCACACCCAC TCATACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT    2546

CCCCTCCCCA TTTGTAAATA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG    2606

AAAAGATTTC CCCTTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGGAACA GGAGAGTCCC    2666

CGGAATCTAG GACCCTAGTC TTTGTACTTG ATGCCTTGTT TCCCCCCTTT TCTTCTTTAA    2726

AATTGGGGAC CTATAACATC ATCGCTGTTG CGGAATCCAC TTAGGCATGT GTCCCCTGAT    2786

GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT    2846

TCCTCTCTCT GGTCCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG    2906

ACACCCTTGC TAGCTTGTCC TGCCTACCTG CTTACCCCAC TCCCTCACCT TCCTCCTTCC    2966

CTTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTTGTAC    3026

ACCCACAGTG GTACCTTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA    3086

TAACTAAACC CTAAACTCTT TTTTGTTGT TGTTGTTGTT GTTTTTTTTT TTTATGATTA    3146

AAAAGTAAAA ATTGTAGTTT AAAAAAAAAA AAAAAAACT CGAG                      3190
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 521 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg
1               5               10              15

Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr
            20              25              30

His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu
        35              40              45

Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met
    50              55              60

Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu
65              70              75              80

His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr
            85              90              95

His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu
        100             105             110

Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu
        115             120             125

Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu
    130             135             140

Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu
145             150             155             160

Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys
            165             170             175

Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro
        180             185             190

Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser
        195             200             205

Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu
    210             215             220

His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro
225             230             235             240

Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His
            245             250             255

Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg
            260             265             270

Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr
    275             280             285

Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn
290             295             300
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Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp
305             310         315             320

Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu
            325             330             335

Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln
            340             345             350

Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr
            355             360         365

Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val
    370             375             380

Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro
385             390             395             400

Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser
            405             410             415

Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr
            420             425             430

Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly
    435             440             445

Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser
    450             455             460

Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser
465             470             475             480

Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His
            485             490             495

Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu
            500             505             510

Leu Glu Arg Arg Val Asn Ala Thr Phe
            515             520
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCT AATGGAGCTG AGAGTCGGG   29

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCG CTCATCGGTG CACGACAGA   29

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 29 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ACAGCTCCAC ATAAGCTGC   29

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAATTCGCT CAAGGAGAGT CCTATTGG   28

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 154 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: (26)...(129)
        (C) OTHER INFORMATION: N = unknown or other

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGTCAGTT CAGCGGATCC TGTCGNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   60

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   120

NNNNNNNNNG AGGCGAATTC AGTGCAACTG CAGC   154

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTCAGTT CAGCGGATCC TGTCG   25

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCAGTTG CACTGAATTC GCCTC   25

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATCGGGCC GCCGAGATCT CATATGGAGC TGAGAGTC   38